Please amend claims 99 and 101 as shown.

Please add new claims 105-112.

Please cancel claims 89-98.

The listing of claims will replace all prior versions and listings of claims in the application.

## Listing of Claims:

1–98 (cancelled)

99. (currently amended)    A    method    of    identifying    a    set    of oligonucleotides    for    use    in    a    physical    recombination    procedure,    the    method comprising:

(a) providing ~~one~~ two or more parental character strings representing one or more polynucleotides or polypeptides, which character strings, when aligned for maximum identity, comprise at least one region of heterology;

(b) aligning the parental character strings;

~~(b)~~ (c) manipulating the one or more parental character strings by applying a ~~genetic~~ crossover operator to computationally generate one or more derivative character strings; and

~~(c)~~ (d) from the one or more derivative character strings, computationally selecting a set of character substrings having sequences that identify the set of oligonucleotides for *in vitro* recombination.

wherein the selected set of character substrings identifies at least one oligonucleotide comprising a chimeric nucleic acid sequence that comprises subsequences from at least two of the parental character strings,

wherein the subsequences from the at least two parental character strings are separated by a crossover point, and

wherein the crossover point is selected from a region outside of an identified pairwise homology region.

100. (previously presented)   The method of claim 99, further comprising:

identifying one or more frame shift mutations or premature terminations among the derivative character strings; and

removing or repairing derivative character strings possessing the one or more frame shift mutations or premature terminations.

101. (currently amended)    The method of claim 99, ~~wherein the~~ further comprising, applying a genetic operator to the one or more parental character strings, wherein the genetic operator is selected from the group consisting of multiplication, mutation, fragmentation, ~~crossover,~~ and ligation.

102 (withdrawn)    A computer program product comprising a machine readable medium on which is provided program code for identifying a set of oligonucleotides for use in a physical recombination procedure, the program code comprising:

(a) code for providing one or more parental character strings representing one or more polynucleotides or polypeptides;

(b) code for manipulating the one or more parental character strings by applying a genetic operator to generate one or more derivative character strings; and

(c) code for selecting a set of character substrings from the one or more derivative character strings, which character substrings have sequences that identify the set of oligonucleotides for in vitro recombination.

103 (withdrawn)    The computer program product of claim 102, further comprising:

code for identifying one or more frame shift mutations or premature terminations among the derivative character strings; and

code for removing or repairing derivative character strings possessing the one or more frame shift mutations or premature terminations.

104 (withdrawn)    The computer program product of claim 102, wherein the genetic operator is selected from the group consisting of multiplication, mutation, fragmentation, crossover, and ligation.

105. (new)    A method of identifying a set of oligonucleotides for use in a physical recombination procedure, the method comprising:

(a) providing two or more parental character strings representing one or more polynucleotides or polypeptides, which character strings, when aligned for maximum identity, comprise at least one region of heterology;

(b) aligning the parental character strings;

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(c) manipulating the one or more parental character strings by applying a crossover operator to computationally generate one or more derivative character strings; and

(d) from the one or more derivative character strings, computationally selecting a set of character substrings having sequences that identify the set of oligonucleotides for *in vitro* recombination.

wherein the selected set of character substrings identifies at least one oligonucleotide comprising a chimeric nucleic acid sequence that comprises subsequences from at least two of the parental character strings,

wherein the subsequences from the at least two parental character strings are separated by a crossover point, and

wherein the crossover point is selected from a region of identified pairwise homology.

106. (new)     The method of claim 105, further comprising:

identifying one or more frame shift mutations or premature terminations among the derivative character strings; and

removing or repairing derivative character strings possessing the one or more frame shift mutations or premature terminations.

107. (new)     The method of claim 105, further comprising, applying a genetic operator to the one or more parental character strings, wherein the genetic operator is selected from the group consisting of multiplication, mutation, fragmentation, and ligation.

108. (new) The method of claim 105, wherein the at least one oligonucleotide comprising a chimeric nucleic acid sequence at least about 10 nucleotides in length.

109. (new) The method of claim 105, further comprising analyzing the one or more derivative character strings with an energy expression.

110. (new) The method of claim 99, wherein the at least one oligonucleotide comprising a chimeric nucleic acid sequence at least about 10 nucleotides in length.

111. (new) The method of claim 99, further comprising analyzing the one or more derivative character strings with an energy expression.

112. (new)    A method of identifying a set of oligonucleotides for use in a physical recombination procedure, the method comprising:

(a) providing two or more parental character strings representing one or more polynucleotides or polypeptides, which character strings, when aligned for maximum identity, comprise at least one region of heterology;

(c) manipulating the one or more parental character strings by applying a crossover operator to computationally generate one or more derivative character strings; and

(d) from the one or more derivative character strings, computationally selecting a set of character substrings having sequences that identify the set of oligonucleotides for *in vitro* recombination.

wherein the selected set of character substrings identifies at least one oligonucleotide comprising a chimeric nucleic acid sequence that comprises subsequences from at least two of the parental character strings, and

wherein the subsequences from the at least two parental character strings are separated by a crossover point.